that to retain a significant HR performance (i.e. lower CI of HR>1) a minimum of 12 of the signature Entrez genes must be selected.

**[0456]** Internal Resection Validation: The average HR performance measured in this dataset using the random sampling of the signature Entrez genes from a feature length of 1 to 30 is shown in FIG. **23**. This figure shows that to retain a significant HR performance (i.e. lower CI of HR>1) a minimum of 7 of the signature Entrez genes must be selected.

**[0457]** The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims. Moreover, all embodiments described herein are considered to be broadly applicable and combinable with any and all other consistent embodiments, as appropriate.

**[0458]** Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

## SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20210254166A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

**1-53**. (canceled)

**54**. A method of treating cancer in a subject comprising:

(a) measuring an expression level of at least one gene selected from CAP6, THBS4, PLP1, MT1A, MIR205HG, SEMG1, RSPO3, AN07, PCP4, ANKRD1, MYBPC, MMP7, SERPINA3, SELE, KRT5, LTF, KIAA120, TMEM158, ZFP36, FOSB, PCA3, TRPM8, PTTG1, PAGE4, STEAP4, TMEM178A, CXCL2, HS3ST3A1, EYA1, RSPO2, PKP1, MUC6, PENK, DEFB1, SLC7A3, MIR578, PI15, UBXN10-AS1, PDK4, PHGR1, SERPINE1, PDZRN4, ZNF185, ADRA2C, AZGP1, TK1, POTEH, KIF11, CLDN1, MIR4530, MAFF, ZNF765, CKS2, TCEAL7, PLIN1, SIGLEC1, FAM15, MFAP5, SFRP1, DUSP5, VARS2, ABCC4, SH3BP4, SORD, MTERFD1, DPP4, FAM3B, KLK3, a gene comprising any one of SEQ ID NOs: 32, 96, 97, 112-114, 120, 121, 132, 141, 149, 185, 186, 210, 211, 213, 214, 221, 264, 328, 329, 344-346, 352, 353, 364, 373, 381, 417, 418, 442, 443, 445, 446 and 453, and a gene comprising any one of SEQ ID NOs: 133 and 365 in a sample from the subject;

(b) providing a signature score based on the measured expression level, wherein the signature score is

(i) a single signature score if the at least one gene consists of one gene, or

(ii) a combined signature score if the at least one gene consists of two or more genes;

(c) determining if the signature score is a positive signature score, wherein the signature score is a positive signature score if

(i) the single signature score is higher than a gene with a positive weight,

(ii) the single signature score is lower than a gene with a negative weight, or

(iii) the combined signature score is equal to or higher than a pre-determined threshold score;

wherein a positive signature score indicates an increased likelihood of recurrence and/or an increased likelihood of metastasis and/or a poor prognosis;

(e) treating the subject who has a positive signature score with one or more of an anti-hormone treatment, a cytotoxic agent, a biologic, radiotherapy, a targeted therapy, or surgery.

**55**. The method of claim **54**, wherein the anti-hormone treatment comprises bicalutamide and/or abiraterone

**56**. The method of claim **54**, wherein the cytotoxic agent is selected from cisplatin, carboplatin, oxaliplatin, paclitaxel, and docetaxel.

**57**. The method a claim **54**, wherein the biologic is Sipuleucel-T.

**58**. The method of claim **54**, wherein the radiotherapy is extended-field radiotherapy.

**59**. The method of claim **54**, wherein measuring the expression level of the at least one gene comprises measuring the expression level of all of CAP6, THBS4, PLP1, MT1A, MIR205HG, SEMG1, RSPO3, AN07, PCP4, ANKRD1, MYBPC, MMP7, SERPINA3, SELE, KRT5, LTF, KIAA120, TMEM158, ZFP36, FOSB, PCA3, TRPM8, PTTG1, PAGE4, STEAP4, TMEM178A, CXCL2, HS3ST3A1, EYA1, RSPO2, PKP1, MUC6, PENK, DEFB1, SLC7A3, MIR578, PI15, UBXN10-AS1, PDK4, PHGR1, SERPINE1, PDZRN4, ZNF185, ADRA2C, AZGP1, TK1, POTEH, KIF11, CLDN1, MIR4530, MAFF, ZNF765, CKS2, TCEAL7, PLIN1, SIGLEC1, FAM15, MFAP5, SFRP1, DUSP5, VARS2, ABCC4, SH3BP4, SORD, MTERFD1, DPP4, FAM3B, KLK3, a gene comprising any one of SEQ ID NOs: 32, 96, 97, 112-114, 120, 121, 132, 141, 149, 185, 186, 210, 211, 213, 214, 221, 264, 328, 329, 344-346, 352, 353, 364, 373, 381, 417, 418, 442, 443, 445, 446 and 453, and a gene comprising any one of SEQ ID NOs: 133 and 365.

**60**. The method of claim **54**, further comprising separately determining prostate-specific antigen (PSA) levels and/or a